

**AMENDMENTS TO THE SPECIFICATION:**

Please replace the Title of the application with the following title:

**Micrococcineae Serine Protease Polypeptides and Compositions Thereof**

On page 25 of the specification, line 32, please replace the following paragraph:

Figure 24 ~~[[28]]~~ provides the plasmid map of the pAPDI vector.

On page 58 of the specification, line 27, through page 59, line 4, please replace the following paragraph:

An example of an algorithm that is suitable for determining sequence similarity is the BLAST algorithm, which is described in Altschul, *et al.*, J. Mol. Biol., 215:403-410 (1990). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (~~<http://www.ncbi.nlm.nih.gov/>~~) ([www.ncbi.nlm.nih.gov](http://www.ncbi.nlm.nih.gov/)). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence that either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. These initial neighborhood word hits act as starting points to find longer HSPs containing them. The word hits are expanded in both directions along each of the two sequences being compared for as far as the cumulative alignment score can be increased. Extension of the word hits is stopped when: the cumulative alignment score falls off by the quantity X from a maximum achieved value; the cumulative score goes to zero or below; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLAST program uses as defaults a wordlength (W) of 11, the BLOSUM62 scoring matrix (*See*, Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)) alignments (B) of 50, expectation (E) of 10, M<sup>+</sup>5, N<sup>-</sup>4, and a comparison of both strands.